Do cryptic reservoirs threaten gambiense-sleeping sickness elimination?

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Informal expert group on gambiense HAT reservoirs *

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Abstract

Trypanosoma brucei gambiense causes human African trypanosomiasis (HAT) in West and Central Africa. Between 1990 and 2015, almost 440,000 cases were reported. Thanks to large-scale screening of populations at risk, drug donations and efforts by national and international stakeholders, the epidemic has been brought under control with < 2200 cases reported in 2016. The World Health Organization has set the goals of gambiense-HAT elimination as public health problem for 2020 and interruption of transmission to humans for 2030. Factors that challenge the sustained elimination of gambiense-HAT are latent human infections and possible animal reservoirs, in particular among domestic animals.

93 Recent studies have increased our knowledge on both phenomena but it remains unknown
94 whether they have an impact on the epidemiology of gambiense-HAT, and if they have, how
95 important that impact is in view of the elimination goal. Here, we argue that a better
96 understanding of the contribution of human and putative animal reservoirs to the
97 gambiense-HAT epidemiology is required to inform elimination strategies.

98

Can cryptic reservoirs in humans and animals compromise the sustainable elimination of gambiense-human African trypanosomiasis?

Human African trypanosomiasis (HAT) **(see Glossary)** is caused by two closely related parasites that are transmitted by tsetse flies. *Trypanosoma brucei gambiense* is responsible for the Western and Central African form of the disease and *Trypanosoma brucei rhodesiense* occurs in Eastern and Southern Africa - both forms of the disease are usually fatal if untreated. Between 1990 and 2016, a total of 437,971 cases of gambiense-HAT were reported, with a peak of 37,385 cases in 1998 (http://www.who.int/gho/neglected_diseases/human_african_trypanosomiasis/en/). Thanks to large-scale deployment of a serological screening test (**CATT/*T.b. gambiense***), drug donations and intense efforts by national and international stakeholders, this epidemic has been brought under control with fewer than 2200 cases reported in 2016. This represents a marked reduction in human suffering caused by the disease. Inspired by this progress, the World Health Organization (WHO) has set **elimination** of gambiense-HAT as a target for the near future: elimination as a public health problem by 2020 and the interruption of transmission to humans by 2030 (http://apps.who.int/iris/bitstream/10665/70809/1/WHO_HTM_NTD_2012.1_eng.pdf).

The rationale to shift from HAT control to elimination is based on several arguments, such as the epidemiological vulnerability of gambiense-HAT as a presumed **anthroponotic** infection, historic examples of elimination in several West African foci, the availability of medicines and diagnostics, the political will of endemic countries and the commitment of national control programs [1]. Furthermore, a drug donation agreement between pharmaceutical companies and WHO has made treatment freely available to endemic countries.

Gambiense-HAT control classically relies on 3 pillars: vector control, diagnosis and treatment. HAT is a vector-borne disease, and the reduction of human-fly contact below a critical threshold would lead to zero transmission. Although vector control is critical to achieve the elimination/eradication goals, it will not be practical to sustainably control all tsetse fly populations in all endemic countries. Vector control being only part of the solution, gambiense-HAT control will continue to rely to a great extent on diagnosis and treatment, both for reducing transmission and for monitoring progress towards these goals.

The introduction of individual **rapid diagnostic tests** (RDTs) for gambiense-HAT may increase serological screening coverage, as they can be performed in remote dispensaries devoid of technical facilities. Thus, they facilitate integration of passive screening in the health system and assist in establishing a sustainable surveillance system. However, RDTs also have limitations - like CATT/*T.b. gambiense*, they only detect antibodies, and their **specificity** is not 100% [2]. As a consequence, given the adverse effects and logistic constraints of current treatment, individuals who test positive in an RDT or in CATT must undergo microscopic examination of blood or lymph node fluid to confirm the presence of the parasite, followed by a lumbar puncture for **stage determination** as different drugs are required to treat early and late stage disease [1]. In recent years, the highly toxic melarsoprol regimen, used to treat late stage disease, has been replaced by a safer though still rather complex treatment, requiring parenteral administration and hospitalisation. An oral treatment might become available in late 2018 and a single-dose treatment is entering phase III clinical trials (http://www.dndi.org/diseases-projects/hat/portfolio/).

Whereas HAT **elimination as a public health problem** by 2020 seems within reach, the sustained global **elimination** of HAT appears more challenging. Indeed, as long as the

145 knowledge gaps surrounding the **reservoir** of *T.b. gambiense* in inter-epidemic periods are
146 not filled, the concept of **eradication** of gambiense-HAT cannot be considered.

147 We present the current research evidence about potential human and animal *T.b.*
148 *gambiense* reservoirs and discuss their importance in the light of the gambiense-HAT
149 elimination goals.

150 **Human reservoir**

151 Mathematical models show that the sustained transmission of HAT can be explained if a
152 fraction of the HAT cases are systematically missed by the screening operations [3].
153 Unfortunately, this is the case in many settings, as a number of *T.b. gambiense* infections
154 remain undiagnosed for several reasons [4]. First, not all infected people are reached by
155 screening activities. Second, actually applied diagnostic techniques do not pick up all *T.b.*
156 *gambiense* infections due to lack of sensitivity of serological screening tests, molecular
157 techniques or of the parasitological confirmation tests [5]. These undiagnosed, yet infected
158 people, will act as a human reservoir of the parasite and might sustain transmission, forming
159 a **maintenance population** [6]. Still another potential category of human reservoir may
160 consist of **latent infections**, also called 'healthy carriers', who do not always progress to
161 clinical disease, though the relative contribution of these individuals to parasite
162 transmission still needs to be documented (BOX 1). These latently infected people may carry
163 trypanosomes for years or even decades, as was first described half a century ago in West
164 Africa and later in patients refusing treatment in Côte d'Ivoire [7,8]. More recently, a HAT
165 case with a latent infection of at least 29 years was documented [9]. In Guinea,
166 asymptomatic or latent infections were found to have consistently high titres in CATT/*T.b.*
167 *gambiense* and to be positive in the **immune trypanolysis** test, although no parasites could

be detected in blood or lymph node fluid during a two-year follow-up period [10]. This observation is in line with the fact that trypanosomes can survive in the extravascular spaces of diverse organs such as the heart, the central nervous system and the skin [11-13]. Experimental infections in animals confirmed that parasites may be undetectable in the blood but hidden in different organs and tissues, [14-17] including the skin, from where they can be ingested by tsetse flies [18,19]. It is only recently that researchers began to investigate the underlying host-parasite interaction mechanisms responsible for those latent infections. Microsatellite profiles and genomic sequencing of parasites from latent infections and from clinical HAT patients are indistinguishable, suggesting that the latent infection phenotype is determined primarily by the host rather than by the parasite [20]. Studies on host genetic polymorphism show that *TNFA-308 A, HLA-G UTR-2, APOL1 N264K and APOL1 G2* are associated with increased risk of infection or with disease progression, while *IL10*$_{-592}$ *A, IL6*$_{4339}$, *APOL1 G1* and other polymorphisms in *HRP and APOL1* are associated with decreased risk of infection or with latent infection [21-26]. Other studies have found associations between the innate and the adaptive immune response and infection outcome, e.g. **self-cure** and high levels of IL8; latent infection and high levels of IL6 or specific IFNG producing T cells; disease progression and high levels of IL10, TNFA and sHLA-G [27-29]. In view of the global elimination of HAT, it is of utmost importance to clarify the extent to which these human reservoirs contribute to the transmission of the parasite and hence to gambiense-HAT persistence and potential resurgence.

Animal reservoir

Compared to latent infections in human, our current knowledge on *T.b. gambiense* infections in animals is very limited and fragmented. The presence of *T.b. gambiense* in

191 animals has been demonstrated in a number of studies (Figure 1) [30,31]. Several authors
192 have suggested that animals can act as a reservoir for gambiense-HAT [32-41]. In
193 rhodesiense-HAT, sustained parasite transmission cycles exist in both livestock and wildlife,
194 from which the parasite can spill over to humans [42]. For *T.b. gambiense*, despite early data
195 generated on its infectivity and transmissibility in animals, the epidemiological significance of
196 any animal reservoir is not well understood and may depend on the specific ecosystem of
197 the **HAT focus**. Even if the parasite can be transmitted to and from animals, factors such as
198 the proportion of blood-feeding on that species by tsetse, will determine the epidemiological
199 significance of the species to act as a maintenance population or part of a **maintenance**
200 **community.** *T.b. gambiense* can infect a variety of domestic animals and wildlife as shown in
201 Table 1. Following infection, most of these animals remain asymptomatic and generally show
202 low to very low parasitaemia. For instance, in pigs infected with a *T.b. gambiense* strain
203 isolated from a human patient, only **xenodiagnosis** and blood culture succeeded in revealing
204 an infection but conventional microscopy failed to detect parasites [43-47]. Moreover,
205 experimental studies have shown that human-derived *T.b. gambiense* strains that were
206 cyclically transmitted by tsetse flies between animals for more than a year, remained
207 transmissible to humans [44].

208 Studying natural *T.b. gambiense* infections in animals is challenging. Major drawbacks are
209 the usually low parasitaemia and the necessity to distinguish *T.b. gambiense* from other
210 trypanosome species such as *T. brucei brucei, T. congolense*, *T. vivax*, *T. suis,* and *T. simiae*. In
211 particular, *T.b. gambiense* is morphologically identical to the non-human infective *T.b.*
212 *brucei.* Among the molecular tests, only those targeting the single-copy TgsGP gene are
213 *gambiense*-specific thus limiting its analytical sensitivity to >100 trypanosomes per ml of

214 blood [48,49]. Biochemical assays such as isoenzyme profiling are only applicable on parasite
215 strains that have been isolated and adapted to laboratory rodents or to *in vitro* cultures [50-
216 52] and phenotypic assays such as the **Blood Incubation Infectivity Test** are only readily
217 applicable on isolated strains and are not fully *gambiense*-specific [53]. Tests that detect
218 antibodies against *gambiense*-specific antigens such as the **Variant Surface Glycoproteins**
219 (VSG) LiTat 1.3 and LiTat 1.5 may be more useful in revealing *T.b. gambiense* infections in
220 animals. However, the immune trypanolysis test (TL) which is considered 100% specific in
221 humans still has to be validated in different species of animals. Ancillary information on the
222 *T.b. gambiense* animal reservoir can be drawn from analysing *T.b. gambiense* infection in
223 tsetse, in combination with its feeding behaviour to assess the vectorial transmission of the
224 parasite from the animal reservoir to humans [54]. In summary, there is a need to further
225 improve our tools and increase our understanding regarding the importance of an animal
226 reservoir in gambiense-HAT epidemiology. If further evidence indicates that an animal
227 reservoir may threaten gambiense-HAT elimination, synergy with the control of animal
228 African trypanosomiasis should be considered [55].

229 **Filling the knowledge gaps**

230 The presence of a reservoir is a critical obstacle to the sustained elimination of any infectious
231 agent [56]. For example, when the Guinea worm eradication programme was rolled out, the
232 possibility of an animal reservoir was initially overlooked, but the recent finding of Guinea
233 worm infections in dogs led to the hypothesis that dogs could have acted as a reservoir that
234 caused the reappearance of human cases in Chad [57]. The existence of a human reservoir,
235 in the form of post-kala-azar dermal leishmaniasis and possibly also latent infections, is a

major challenge for the sustained elimination of visceral leishmaniasis (VL) from the Indian subcontinent [58].

The importance of investigating how HAT can re-emerge in so-called silent foci is clearly illustrated by the fact that a nine-year old child was diagnosed with gambiense-HAT in Ghana in 2013, ten years after the last detected case [59]. Also, the finding of a *gambiense*-specific PCR positive squirrel in Equatorial Guinea on Luba island in 2014 where the last human HAT case was reported in 1995 is worrying [39]. Therefore, in the context of gambiense-HAT elimination, a key question is whether human and/or animal reservoirs are capable of maintaining transmission and causing resurgence of the disease in different geographical areas and epidemiological settings (**see Outstanding Questions**).

As with the mathematical modelling of other neglected tropical diseases [60], models on HAT epidemiology may help to improve our epidemiological knowledge and inform elimination strategies. Models can explore if, and how, animal and human reservoirs could sustain endemicity in HAT foci [61]. However, model predictions heavily depend on the availability of accurate information for their construction, parameterisation and fitting. To date, a few models have attempted to infer the contribution of reservoirs in gambiense-HAT transmission maintenance by fitting to human epidemiological data. Funk *et al.* [74] suggested that animals were necessary for persistent transmission in Bipindi focus in Cameroon. Studies of existing gambiense-HAT models in a few foci (i.e. D.R. Congo, Guinea and Chad) suggest that some type of additional infection reservoir is needed to match the observed dynamics of reported HAT cases [3,62,63]. This could arise from another human reservoir (including undiagnosed and latent infections), an animal reservoir and/or heterogeneities in human risk exposure and surveillance coverage. A different modelling

exercise considered the implications on transmission and control of whether animals function as reservoirs or as zooprophylaxis but did not address which was more likely [64]. Due to the current lack of knowledge surrounding latently infected people (including their frequency, disease progression, their relative infectivity to tsetse and the duration of this infectious stage) modelling latent infections in humans is challenging, and these uncertainties will impact the models' predictions. In particular, latent infections have only been explicitly incorporated in one gambiense-HAT model and the potential role of these individuals in maintaining transmission or hindering elimination has yet to be fully analysed [65]. Arguably long duration infections, which eventually progress to late stage disease, are captured by the stage 1 exponential distributions used in many modelling frameworks, but modifications could better represent self-cure and non-detection of latent infections in active screening. Many recent modelling studies have concluded existing vector control methods have the ability to quickly reduce transmission to and from tsetse to all hosts and may be critical for elimination in regions where reservoirs exist [62-67].

New data and investigations into latent human infections and animal infections will help shape the way in which future models are developed and parameterised by factoring in improved biological evidence. Some key gaps in our knowledge, which influence modelling choices, are shown in **Figure 2, Key Figure**. As well as refining formulation and parameterisation of the existing **deterministic** models, it is also clear that a new generation of models is needed. **Stochastic models** are better suited to capture the chance events that determine the role of cryptic reservoirs and their implications for elimination. In conclusion, improved mathematical models on HAT epidemiology combined with additional field and experimental data are needed to help understand the respective roles of these reservoirs.

Concluding remarks

We believe that attaining the elimination (zero transmission) target of gambiense-HAT by 2030 is feasible but, as observed for other neglected tropical diseases, latent infections - whether human or animal - may constitute cryptic parasite reservoirs and thus add another challenge to sustained elimination. To inform evidence-based elimination strategies, a better understanding of the contribution of these putative human and animal reservoirs on the epidemiology of gambiense-HAT is required, more in particular on (1) the frequency and duration of latent human infections and infections in animals, (2) the infectiveness of latent human infections and animal reservoirs to tsetse flies, (3) the ability of latent human infections or animal reservoirs to sustain transmission in inter-epidemic periods, and (4) the possible existence of an animal transmission cycle in the absence of human transmission and its ability to seed a new transmission cycle in humans. To investigate these issues, we urgently need to improve our toolbox for the identification of latent and self-cured infections, including prognostic and diagnostic markers. Also, more accurate and preferably high-throughput tests to detect and monitor *T.b. gambiense* infections in animals should be developed, along with improved mathematical models for exploration of epidemiological hypotheses.

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494

492 **Table 1: Animals successfully infected with *T.b. gambiense* strains isolated from human patients.**

Animal species	**Origin of trypanosome strain[a]**	**Infectiveness to tsetse**	**Minimum observed duration of infection**	**References**
Domestic animals				
Cat	Senegambia and Congo Free State	Not tested	12 days	[68]
Cattle	Nigeria	Yes	50 days	[69,70]
Chicken	Unknown	Not tested	75 days	[71]
Dog	Senegambia and Congo Free State, Nigeria; Belgian Congo	Yes	109 days	[32,44,68]
Donkey	Senegambia	Not tested	14 days	[68]
Goat	Senegambia, Nigeria, Belgian Congo	Yes	13 months	[44,68,69]
Horse	Senegambia	Not tested	5 months	[68]

Pig	Côte d'Ivoire, Congo Belge, Nigeria	Yes	18 months	[43,47,72]
Sheep	Côte d'Ivoire	Not tested		[73]
Primates				
Agile mangabey *(Cercocebus galeritus agilis)*	Belgian Congo	Yes		[44]
Green monkey *(Cercopithecus callitrichus, C. aethiops tantalus)*	Congo Free State, Nigeria	Yes	3 months	[32,68]
Wolf's mona monkey *(Cercopithecus wolfi)*	Congo Belge	Yes	15 days	[43]
Patas monkey *(Erythrocebus patas patas)*	Nigeria	Yes	3 months	[32,74]
Rhesus macaque *(Macacus rhesus)*	Senegambia and Congo Free State	Not tested	1 month	[68]

Chimpanzee *(Pan satyrus, Pan troglodytes verus)*	Senegambia, Nigeria	Not tested	17 months	[68,74,75]
Dwarf galago *(Galagoides demidovii)*	République populaire du Congo	Not tested	28 days	[76]
Ungulates				
Bay duiker *(Cephalopus dorsalis)*	Belgian Congo	Yes	24 months	[44]
Waterbuck *(Kobus ellipsiprymnus)*	Uganda	Not tested		[46]
Reedbuck *(Redunca redunca)*	Uganda	Yes	15 months	[46]
Bushbuck *(Tragelaphus spekei)*	Uganda	Yes	22 months	[46]
Rodents				
Gambian pouched rat *(Cricetomys gambianus)*	République populaire du Congo	Yes	154 days	[33,76,77]
Thicket rat *(Thamnomys rutilans),* Jackson's praomys *(Praomys jacksoni),* African marsh rat *(Dasymys*	République populaire du Congo	Not tested	131 days	[76]

	incomtus), Striped grass mouse *(Lemniscomus striatus),* Rusty-nosed rat *(Cenomys hypoxanthus),* African brush-tailed porcupine *(Atherurus africanus)*

493 [a] For reasons of traceability, we use the name of countries and the scientific name of animals as mentioned in the original publication: Senegambia = Senegal and

494 The Gambia; Belgian Congo, Congo Free State and Congo Belge = Democratic Republic of the Congo; République populaire du Congo = Republic of the Congo.

495

Box 1: Diversity in outcomes of human *Trypanosoma brucei gambiense* infections

There is growing evidence that infection with *T.b. gambiense* does not always follow the classical course of the disease, i.e. a first haemo-lymphatic stage followed by a second stage with central nervous system involvement progressing to death if left untreated (see Figure I). These symptomatic **HAT patients** are characterised by the detection of parasites in any body fluid (P+), detection of specific antibodies against *T.b. gambiense* Variable Antigen Type LiTat 1.3 or LiTat 1.5 in immune trypanolysis (TL+), and the presence of clinical symptoms. However, long-term follow-up studies in West Africa have shown that a number of infected individuals do not develop the disease and can be classified as having **latent infections** (*i.e.* they are healthy carriers) [7]. They remain asymptomatic without detectable parasites (P-) for several years, although they are consistently positive in the immune trypanolysis test (TL+). Moreover, some of them may become immune trypanolysis negative (TL-) over time suggesting that they **self-cured** and therefore cannot transmit the parasite anymore.

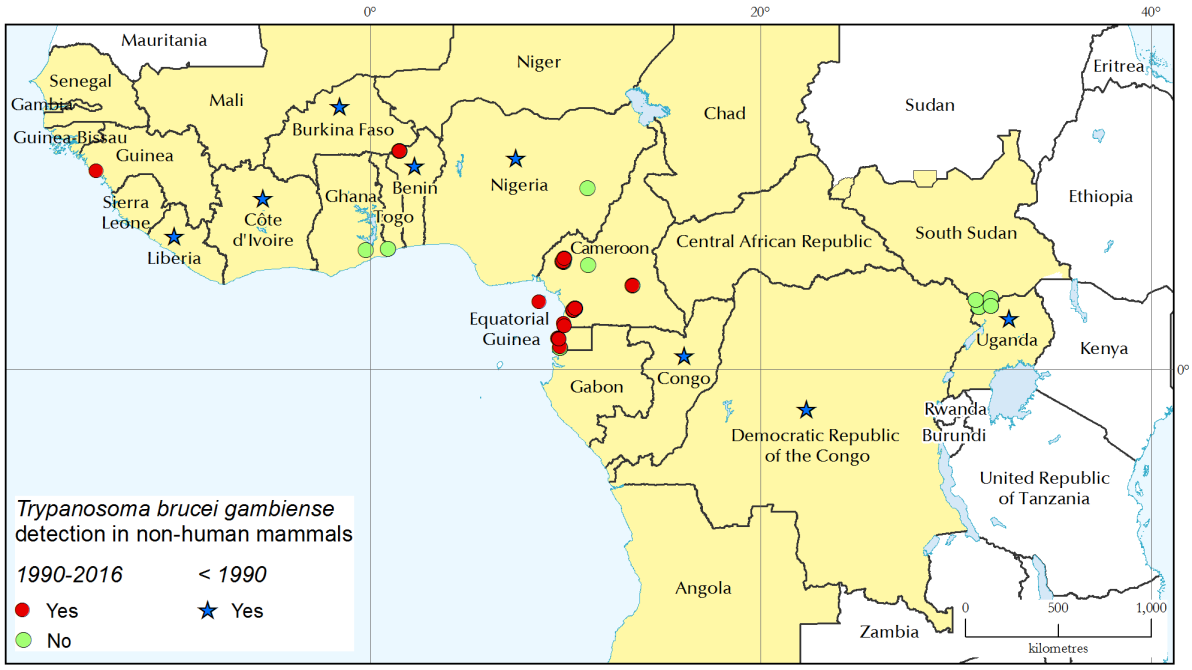
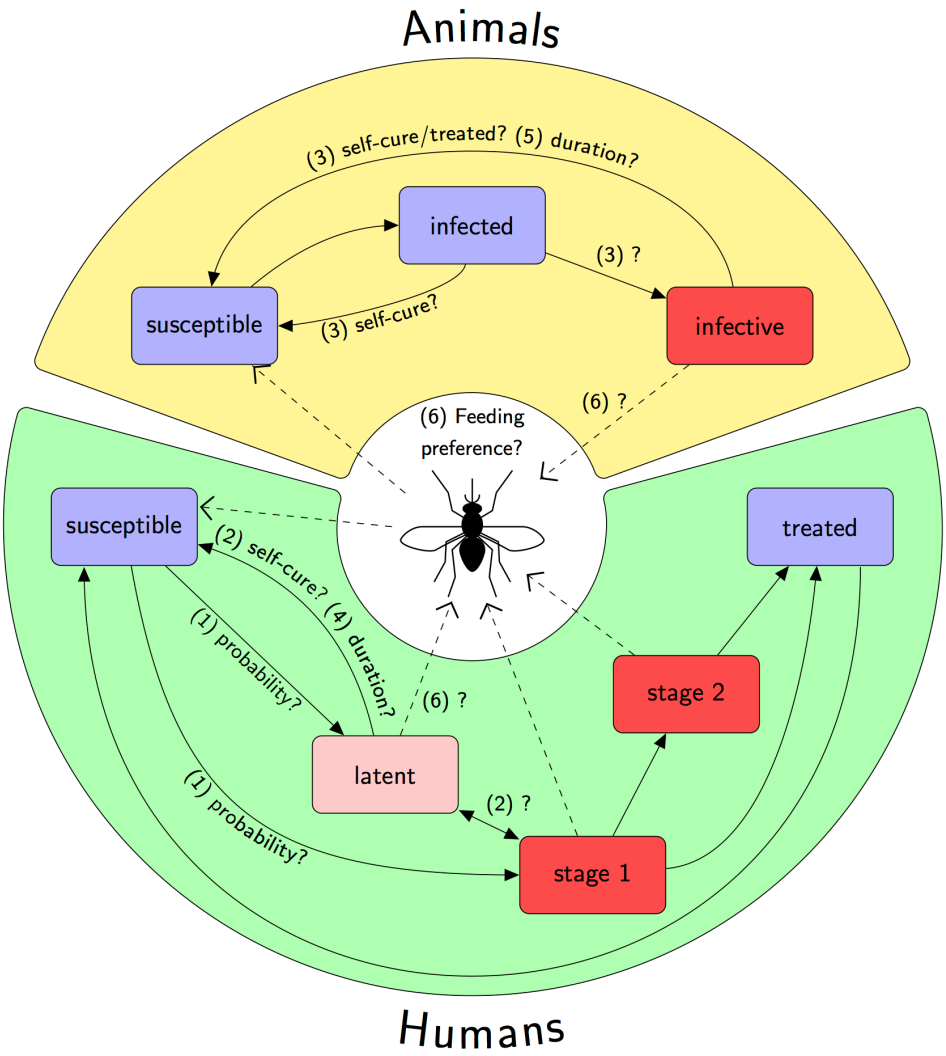


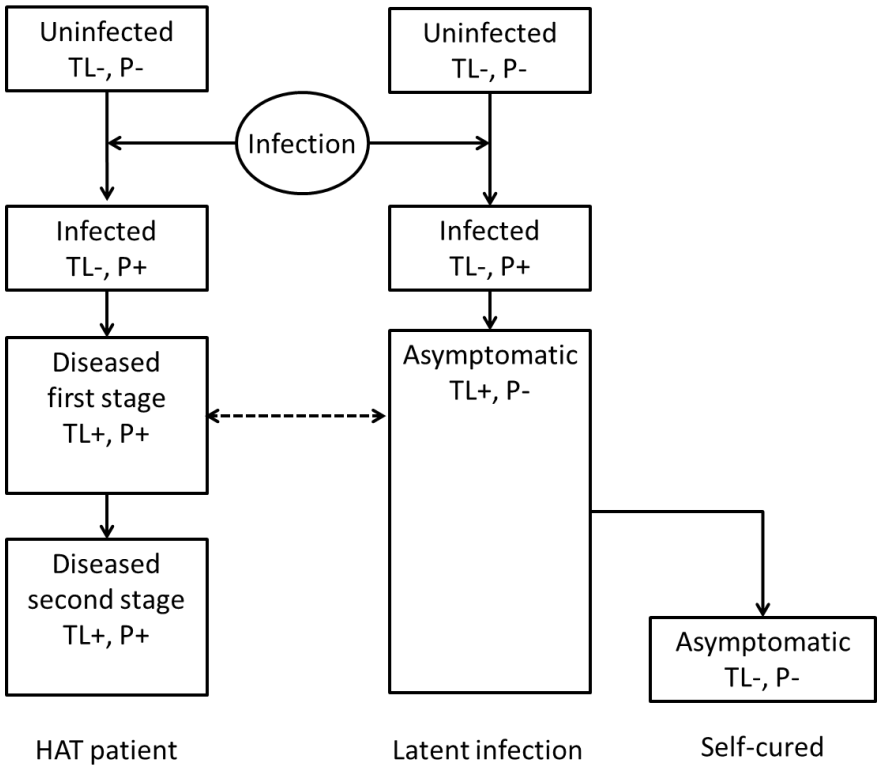
Figure 1: *Trypanosoma brucei gambiense* in non-human mammals. Map showing gambiense-human African trypanosomiasis in endemic countries and sites where *T. b. gambiense* infection in non-human mammals has been investigated with direct and indirect methods. Circles represent direct or indirect evidence of presence (red) and of absence (green) of *T.b. gambiense* in the period 1990-2016. For this period, data are mapped at the village/site level. (Blue) stars represent presence of detection in the years prior to 1990. For this period, data are mapped at the country level. All source references are provided as Supplemental Information.



521

522 **Figure 2, Key Figure: Unknown elements in human African trypanosomiasis progression**
523 **and transmission.** Solid lines represent progression between disease states, and dashed
524 lines represent transmission of the parasites to and from the tsetse vector. Red boxes
525 denote people or animals that may be infective to tsetse, with the darker shades denoting
526 possible greater infectiveness. The figure highlights key unknown elements in disease
527 progression and transmission including: (1) the probability of an infection leading to latent
528 or stage 1 disease in humans; if, and how frequently, (2) self-cure of infected humans or (3)
529 animals arises, (4) the duration of latent infection in humans or (5) any infections in animals,

530 and (6) the relative probability of transmission to tsetse from different types of infections
531 (accounting for host feeding preferences).



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534 **Figure I (Box 1): Outcomes of human infection with *Trypanosoma brucei gambiense*.**
535 When naïve persons (Uninfected), without specific antibodies (TL-) and without parasites (P-
536) get infected with *T.b. gambiense*, they undergo an early phase of the disease with
537 detectable parasitaemia (P+) but without detectable specific antibodies. Thereafter, most of
538 them develop the disease (HAT patient) and are characterised by specific antibodies (TL+)
539 and detectable parasitaemia (P+). Some remain asymptomatic (Latent infection) with
540 detectable specific antibodies but without detectable parasites (TL+, P-). Evidence for self-
541 cure comes from asymptomatic people that also eventually become negative for specific
542 antibodies (TL-, P-).

543

544

Glossary

Anthroponotic disease: an infectious disease typically transmitted from human to human (including through an insect vector).

Blood Incubation Infectivity Test: *T.b. gambiense* and *T.b. rhodesiense* have developed mechanisms to withstand lysis by normal human serum, in contrast with animal infective trypanosomes like *T.b. brucei*, *T. congolense*, *T. vivax*. To confirm that an animal is infected with *T.b. gambiense* or *T.b. rhodesiense*, its blood, or trypanosomes isolated from that animal, are incubated with human blood or serum where after this mixture is injected in a susceptible animal. Only human serum resistant trypanosomes will be able to initiate an infection in the susceptible animal.

CATT/*T.b.gambiense*: Card Agglutination Test for Trypanosomiasis is an agglutination test for detection of gambiense-specific antibodies in blood. It was the first field-applicable serological test introduced in the 1980s for large-scale screening of populations at risk for gambiense-HAT.

Deterministic mathematical model: Deterministic models ignore the impact of random events, instead capturing average disease dynamics, so that multiple simulations with the same parameter values and initial conditions will lead to exactly the same outcome.

Elimination of gambiense-HAT: Elimination is the reduction to zero of gambiense-HAT incidence in a defined area as a result of deliberate efforts; measures to prevent re-emergence are required.

Elimination of gambiense-HAT as a public health problem: 90% reduction in areas reporting more than 1 case in 10,000 compared to 2000-2004, and fewer than 2,000 annually reported cases globally**.**

568 **Eradication of gambiense-HAT:** Eradication is the permanent reduction to zero of the
569 worldwide incidence of gambiense-HAT as a result of deliberate efforts; intervention
570 measures are no longer needed.
571 **HAT focus:** A geographically defined zone where transmission of HAT occurs or has
572 occurred, to which a geographical name is given (locality, region and river).
573 **Immune trypanolysis**: Highly accurate test for gambiense-specific antibodies, based on
574 antibody-mediated complement lysis of trypanosomes exposing one single variant-specific
575 antigen on their surface.
576 **Latent infection:** On-going infection not progressing to clinical disease, that may remain
577 undiagnosed.
578 **Maintenance community**: One or more populations which can transmit the pathogen and,
579 together, can maintain the pathogen
580 **Maintenance population**: Individual populations which can transmit the pathogen and can
581 also maintain the pathogen in the absence of other reservoir populations.
582 **Rapid diagnostic test (RDT):** Serological antibody or antigen detection test, conditioned as
583 individual test, compliant with the ASSURED criteria (Affordable, Sensitive, Specific, User-
584 friendly, Rapid and robust, Equipment-free and Deliverable to end-users); RDTs for
585 gambiense-HAT detect antibodies against predominant gambiense-specific antigens.
586 **Reservoir:** Host where the pathogen can maintain itself and from where it can be
587 transmitted to another host; a reservoir host is essential to sustain infection.
588 **Self-cure:** Infection that is cleared by the host without treatment.
589 **Specificity:** The specificity of a diagnostic test is the probability that the test result is
590 negative when the test person is not infected. It is usually expressed as percentage and
591 calculated by dividing the number of test negatives by the number of true negatives x 100.

Stage determination: HAT develops from an early stage with parasites in the peripheral tissues towards a late stage with parasite invasion into the central nervous system. Treatment is different for both stages, thus requiring stage determination before drug administration. Determination of the stage is achieved by examination of the cerebrospinal fluid for the presence of trypanosomes and the number of white blood cells.

Stochastic mathematical model: Stochastic models include chance events so that two simulations with the same parameter values and initial conditions may lead to different outcomes. Chance events become more important at very low prevalences such as in pre-elimination or re-emergent settings.

Variant Surface Glycoprotein (VSG): In the vertebrate host, the cell surface of trypanosomes is covered with a layer of identical VSGs of one particular variant antigen type (VAT), that protects the trypanosomes against innate immune defence mechanisms of the host; VSGs are highly immunogenic but periodic switches of the VAT of the VSG coat (antigenic variation) enable the trypanosome to escape the host humoral immune response; during the course of the infection, the host blood contains antibodies against a wide spectrum of different VATs.

Xenodiagnosis: Diagnostic method based on detection of the parasite in susceptible vectors after they were fed on an individual suspected of being infected with the parasite; in HAT, the vectors used are teneral tsetse flies.